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Search Results -

Terms	Documents
L3 and (dual with specific$)	5

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Search: L4

Refine Search | Recall Text | Clear

Search History

DATE: Thursday, November 07, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=NO; OP=OR			
L4	L3 and (dual with specific$)	5	L4
L3	L1 and (antisense or ribozyme$) and phosphatase$	34	L3
L2	L1 same (antisense or ribozyme$)	0	L2
L1	hvh3 or b23 or dusp5	1522	L1

END OF SEARCH HISTORY

Set	Items	Description
S1	0	(DUSP (W) 5)
S2	23	HVH (W) 3
S3	5	RD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

3/3,K/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

11605962 BIOSIS NO.: 199800387697

Changes of gene expression by lysophosphatidylcholine in vascular endothelial cells: 12 Up-regulated distinct genes including 5 cell growth-related, 3 thrombosis-related, and 4 others.

AUTHOR: Sato Naoaki; Kokame Koichi; Shimokado Kentaro; Kato Hisao; Miyata Toshiyuki(a)
AUTHOR ADDRESS: (a)Natl. Cardiovasc. Cent. Res. Inst., 5-7-1 Fujishirodai, Suita, Osaka 565-8565**Japan

JOURNAL: Journal of Biochemistry (Tokyo) 123 (6):p1119-1126 June, 1998
ISSN: 0021-924X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

QP 501 .J6

...ABSTRACT: and untreated human umbilical vein endothelial cells. We identified 12 up-regulated distinct genes including 5 cell growth-related genes (two phosphatases CL100 and B23/*hVH*-*3*, gravin, activating transcription factor-4, and heparin-binding epidermal growth factor-like growth factor), 3 thrombosis-related genes (plasminogen activator inhibitor-1, tissue plasminogen activator...

3/3,K/2 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

10026345 BIOSIS NO.: 199598481263

The role of dual specificity phosphatase *HVH*-*3* on ERK regulation during neuronal differentiation.

AUTHOR: Kwak S P; Dixon J E
AUTHOR ADDRESS: Dep. Biol. Chem., Univ. Michigan, Ann Arbor, MI 48109**USA

JOURNAL: Society for Neuroscience Abstracts 21 (1-3):p808 1995
CONFERENCE/MEETING: 25th Annual Meeting of the Society for Neuroscience San Diego, California, USA November 11-16, 1995
ISSN: 0190-5295
RECORD TYPE: Citation
LANGUAGE: English

The role of dual specificity phosphatase *HVH*-*3* on ERK regulation during neuronal differentiation.

3/3,K/3 (Item 3 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

09665875 BIOSIS NO.: 199598120793

Multiple dual specificity protein tyrosine phosphatases are expressed and regulated differently in liver cell lines.

QP 501 .J7
or
M Online

AUTHOR: Kwak Seung P; Dixon Jack E(a)
AUTHOR ADDRESS: (a)Dep. Biol. Chem., Room 5416, Med. Sci. Building 1, University Michigan, Ann Arbor, MI 48109-0606**USA

JOURNAL: Journal of Biological Chemistry 270 (3):p1156-1160 1995
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

↓ 269 : 29,897 – 29,902

...ABSTRACT: other PTPases they exhibit dual catalytic activity toward phosphotyrosine and nearby phosphothreonine residues in substrate proteins. We have isolated a novel VH-1-like PTPase, *hVH*-*3*, from the human placenta and compared various aspects of its expression with previously isolated members of this subfamily. The mammalian members of this subfamily including *hVH*-*3* commonly localize to the nucleus and exhibit catalytic activity toward phosphorylated extracellular signal-regulated kinase. However, while the expression of some VH-1-like PTPases is extremely transient and independent of protein synthesis, *hVH*-*3* expression is sustained over 3 h after being cell stimulated. Tissue-specific expression of *hVH*-*3* is also distinct from other VH-1-like PTPases. Although VH-1-like PTPases have overlapping substrate specificity, there are differences in their mRNA regulation...

3/3,K/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09410228 BIOSIS NO.: 199497418598
Chromosomal localization of four human VH1-like protein-tyrosine phosphatases.
AUTHOR: Martell Karen J; Kwak Seung; Hakes David J; Dixon Jack E(a); Trent Jeffrey M
AUTHOR ADDRESS: (a)Dep. Biol. Chemistry, University Michigan Med. Center, 5416 Med. Science Building I, Ann Arbor, **USA
JOURNAL: Genomics 22 (2):p462-464 1994
ISSN: 0888-7543
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

QH426.G46

...ABSTRACT: genes were localized to unique regions of different chromosomes: CL100, a stress-induced PTPase, to 5q35; PAC-1, a mitogen-induced nuclear PTPase, to 2q11; *hVH*-*3* to 10q25; and hVH-4 to 10q11.

3/3,K/5 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

03724792 Genuine Article#: QB156 No. References: 30
Title: MULTIPLE DUAL-SPECIFICITY PROTEIN-TYROSINE PHOSPHATASES ARE EXPRESSED AND REGULATED DIFFERENTIALLY IN LIVER-CELL LINES
Author(s): KWAK SP; DIXON JE
Corporate Source: UNIV MICHIGAN,DEPT BIOL CHEM,RM 5416,MED SCI BLDG 1/ANN ARBOR//MI/48109; UNIV MICHIGAN,DEPT BIOL CHEM/ANN ARBOR//MI/48109
Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1995, V270, N3 (JAN 20), P 1156-1160
ISSN: 0021-9258
Language: ENGLISH Document Type: ARTICLE (Abstract Available)

...Abstract: other PTPases they exhibit dual catalytic activity toward phosphotyrosine and nearby phosphothreonine residues in substrate proteins. We have isolated a novel VH-1-like PTPase, *hVH*-*3*, from the human placenta and compared various aspects of its expression with previously isolated members of this subfamily. The mammalian members of this subfamily including *hVH*-*3* commonly localize to the nucleus and exhibit catalytic activity toward phosphorylated extracellular signal-regulated kinase. However, while the expression of some VH-1-like PTPases is extremely transient and independent of protein synthesis, *hVH*-*3* expression is sustained over 3 h after being cell stimulated. Tissue-specific expression of *hVH*-*3* is also distinct from other VH-1-like PTPases. Although VH-1-like PTPases have overlapping substrate specificity, there are differences in their mRNA regulation...

Set Items Description
S1 0 (DUSP (W) 5)
S2 23 HVH (W) 3
S3 5 RD (unique items)
S4 294 B23 AND PHOSPHATASE?
S5 48 S4 AND (NUCLEIC (W) ACID?)
S6 48 RD (unique items)
S7 45 S6 AND SEQUENCE?
S8 4 S7 AND THREONINE? AND TYROSINE?
>>>KWIC option is not available in file(s): 41, 77, 399

8/3,K/1 (Item 1 from file: 370)
DIALOG(R)File 370:Science

00509950 (USE 9 FOR FULLTEXT)
Type III Secretion Machines: Bacterial Devices for Protein Delivery into Host Cells
Galan, Jorge E.<CRF RID="C1"> ; Collmer, Alan
Section of Microbial Pathogenesis, Boyer Center for Molecular Medicine, Yale School of Medicine, New Haven, CT 06536, USA. Department of Plant Pathology, Cornell University, Ithaca, NY 14853-4203, USA.
Science Vol. 284 5418 pp. 1322
Publication Date: 5-21-1999 (990521) Publication Year: 1999
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: REVIEWS
Word Count: 5376

(THIS IS THE FULLTEXT)

...Text: outer membrane. Consequently, these bacteria have evolved a variety of mechanisms to transfer proteins from the cytoplasm to the extracellular environment (B2) . The discovery of *sequence* homologies between proteins implicated in the secretion of virulence factors in several different bacterial pathogens and proteins implicated in the export of flagellar components prompted...

...often have a GC content that deviates from that of the chromosome of the host organism, and they are usually bounded by remnants of insertion *sequences*, bacteriophage genes, or transposable elements. Amino acid *sequence* comparison of the most conserved components of type III secretion and flagellar export systems shows a clustering of different family members in discrete groups (Fig...highly conserved (B1) . These components can be divided into at least two groups. One group consists of predicted outer membrane proteins, including a protein with *sequence* similarity to the secretin family of protein transporters, as well as several less conserved lipoproteins. The other group consists of several integral membrane proteins with...

...and two lipoproteins, PrgH and PrgK. Despite the architectural similarity between flagella and type III systems, the structural components of the needle complex share limited *sequence* similarity with components of the flagellar basal body (B8) . Although information on the supramolecular organization of type III secretion systems from other bacteria is currently not available, the high degree of *sequence* similarity among several structural components indicates that all these systems are likely to have a similar architecture...
...triphosphate (ATP) hydrolysis provides the energy for the secretion process. This is supported by the observation that a conserved component of the secretion systems shares *sequence* similarity with the a and (beta) subunits of the F1 component of the bacterial F0F1 proton-translocating ATPase and that in at least two systems...signal must reside in the structure of the mRNA because mutations that shifted the reading frame of the putative secretion signal, yielding completely different polypeptide *sequences*, were still able to direct secretion through the type III machinery (B14) . The 5 (prime) mRNA regions of some of the yop messages

are predicted...

...secretion-associated chaperones have a rather narrow binding specificity and appear to lack nucleotide-binding or nucleotide-hydrolyzing activities. Although they exhibit little amino acid *sequence* similarity, type III secretion chaperones share a number of properties such as relatively small size (15 to 18 kD), a low isoelectric point, and a*B23*) .
...

...macrophage function (B13) . YopH appears to exert its effect by dephosphorylating p130.sup(cas) and focal adhesion kinase, two components of focal adhesions that become *tyrosine* phosphorylated upon (beta) 1-integrin stimulation (B27) . Pseudomonas aeruginosa delivers an adenosine diphosphate-ribosylating toxin, ExoS, that targets actin-organizing small guanosine triphosphate (GTP)-binding...

...membrane ruffling, and macropinocytosis, ultimately resulting in bacterial uptake (B29) . The effector proteins include an exchange factor for Rho GTPases (SopE) (B30) , an inositol phosphate *phosphatase* (SopB) (B31) , and an actin-binding protein (SipA) (B32) . SopE acts as an exchange factor for a subset of Rho GTPases, including CDC42 and Rac (B30) . SopB modulates the actin cytoskeleton through its inositol phosphate *phosphatase* activity, which generates a broad range of inositol phospholipids and inositol phosphates with demonstrated signaling capacity (B31) . By binding to actin, SipA decreases its critical...induction of apoptosis is dependent on the function of the type III secreted protein YopJ (YopP), which functions by an unknown mechanism (B37) . YopJ shares *sequence* similarity with effector proteins delivered by type III systems in other bacteria, such as the animal pathogen S. typhimurium (AvrA) as well as the phytopathogen...

...significance because the AvrRxv protein has been implicated in the stimulation of the hypersensitive response in plants, which involves the induction of apoptosis. Whether the *sequence* similarity among these effector proteins points at some basic signaling pathway conserved in both animals and plants is an open question that may be answered...inside plant cells, indirectly supporting the hypothesis that type III secretion systems direct their delivery to that site (B43) . For example, (i) the amino acid *sequence* of R gene products that are expected to interact with Avr proteins predict an intracellular localization, (ii) several Avr proteins elicit an R gene-dependent...was constructed from a distance matrix (by the unweighted pair group method using arithmetic averages) as implemented in the GCG software package (B45) . Names of *sequences* correspond to the entries in GenBank...

...ADP-ribosyltransferase

	ExoT	ADP-ribosyltransferase
	ExoY	Adenylate cyclase
S. typhimurium	SopE	Exchange factor for Rho GTPases (such as CDC42 and Rac)
	SopB (SigA)	Inositol phosphate *phosphatase*
	SipA	Binds actin, lowering its critical concentration and stabilizing F-actin
	SptP	*Tyrosine* *phosphatase*
Shigella spp.	IpaB	Activation of caspase-1; binds (beta) 1-integrins and CD44
	IpaA	Binds vinculin
	IpgD	Putative inositol phosphate *phosphatase*
Yersinia spp.	YopE	Unknown
	YopH	*Tyrosine* *phosphatase*
	YpkA	Serine/*threonine* kinase
	YopJ (YopP)	Unknown
Plant pathogens		
P. syringae pv. tomato	AvrPto	Interacts with Pto (R gene product); activates Pto

		serine/*threonine* kinase signaling pathway
Xanthomonas campestris pv. vesicatoria	AvrBs2	Interacts with Bs2 R gene product of resistant pepper cultivars; *sequence* predicts ability to synthesize or hydrolyze phosphodiester linkages, which may be involved in its virulence function
X. campestris pv. vesicatoria	AvrBs3 family	Localized to plant nuclei; probable transcription factors; activity determined by multiple repeats of 34 amino-acid *sequence*

End Table: Columns 1 - 3 of 4
Begin Table : Columns 4 - 4 of 4

Caption:
Examples of effector proteins of known function secreted...

References and Notes:
...Devereux, J., Haeberli, P., Smithies, O., *Nucleic* *Acids* Res., 12 1984, 387...

8/3,K/2 (Item 2 from file: 370)
DIALOG(R)File 370:Science

00508367 (USE 9 FOR FULLTEXT)
Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence
Chervitz, Stephen A.; Aravind, L.; Sherlock, Gavin; Ball, Catherine A.; Koonin, Eugene V.; Dwight, Selina S.; Harris, Midori A.; Dolinski, Kara; Mohr, Scott; Smith, Temple; Weng, Shuai; Cherry, J. Michael; Botstein, David
S. A. Chervitz, G. Sherlock, C. A. Ball, S. S. Dwight, M. A. Harris, K. Dolinski, S. Weng, J. M. Cherry, and D. Botstein are in the Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305-5120, USA. L. Aravind and E. V. Koonin are at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA. S. Mohr and T. Smith are in the Department of Biomedical Engineering, Boston University, Boston, MA 02115, USA.
Science Vol. 282 5396 pp. 2022
Publication Date: 12-11-1998 (981211) Publication Year: 1998
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Special Section
Word Count: 4794
(THIS IS THE FULLTEXT)

...Abstract: Comparative analysis of predicted protein *sequences* encoded by the genomes of Caenorhabditis elegans and Saccharomyces cerevisiae suggests that most of the core biological functions are carried out by orthologous proteins (proteins...

Text: The nematode worm Caenorhabditis elegans is only the second eukaryote to have its genome completely *sequenced* (B1) . The first complete eukaryotic genome *sequence*, that of the budding yeast Saccharomyces cerevisiae, has been reported previously (B2) . Thus, for the first time, it is possible to compare the entire complements...

...The first result is quite surprising: Simple *sequence* comparisons allow one to predict, more often than not, orthologous pairs. In many cases, orthologous pairs can be confidently delineated even within families

of highly...

...as described in Table 1. The ORFs within each group were then ordered by similarity clustering with the CLUSTALW program (B14) and displayed as multiple *sequence* alignments, rooted cluster dendrograms, and unrooted trees. Each of these displays for every comparison can be found on our Web site. The numbers of worm and yeast ORFs that fall into these clusters at various similarity thresholds are given in Table 1. Figure 1 graphically depicts the distribution of the *sequences* from the worm-yeast clusters within functional categories. The first significant (and somewhat unexpected) observation is that the absolute number of ORFs for which we...
...is not accounted for by endless close variations in the clusters found among the shared set, but instead are proteins that are substantially different in *sequence* [compare with (B15)] and thus are likely to perform tasks that are specific to each organism. A subset of such organism-specific proteins, those associated...

...annotation that exists almost exclusively for yeast) might be transferable to the worm, provided that the orthologs between the two species are easily recognizable by *sequence* analysis alone. Functional conservation of proteins from different species was first demonstrated experimentally by showing that the mammalian RAS protein can substitute for yeast RAS...

...Table 1 shows that at each level of significance roughly half (611 of 1171 at P < 10.sup(-10)) of all the *sequence* similarity groups found by our reciprocal BLASTP procedure contain exactly two members. Because ascertainment of each group began with a yeast-worm HSP, these groups contain one worm and one yeast member. The availability of complete *sequences* for both worm and yeast makes it unlikely that we are missing large numbers of potential orthologs. It remains possible that the conservative similarity cutoffs...
...this instance, most of the cases for pairing are conclusive, because the RNA polymerase I and II subunits were independently identified in yeast and worm (*B23*) . In addition, the cluster [here done at P< 10.sup(-20) (B24)] contains the yeast polymerase III subunit paired with its presumed ortholog in the...of proteasome subunits (B26) . In this case there are 25 members of the cluster, which form 10 clear pairs, with three yeast and two worm *sequences* apparently unpaired. However, it seems probable that there is an additional orthology: yeast PRE2 with the minimally diverged (recently duplicated?) worm *sequences* K05C4.1 and Y105E8A.jj. Accepting this, the 25 *sequences* yield 11 pairs...

...case of the worm apparently missing orthologs for a set of important yeast proteins. Comparisons were performed with PSI-BLAST (B33) and validated by demonstrating *sequence* similarity to Escherichia coli or Methanoccus jannaschii protein *sequences*. A total of 108 mitochondrial proteins from yeast have highly conserved homologs in worm (P-value scores <10.sup(-39)). These orthologous pairs can be...emerge from these results is that annotation of protein functions and activities will be reliably transferable between organisms as disparate as yeast and worm by *sequence* analysis. With well-annotated genomes, the identification of orthologous pairs becomes a powerful analytical approach. Whereas biochemical and biological experiments must be done to unequivocally prove the functions of proteins, the wealth of data from *sequence* analyses allows researchers to better design experiments and avoid duplication of work done in other systems...indicated by the conservation of the entire domain architecture of the SH2-containing transcription factor Spt6p. However, the best known role of SH2, in the *tyrosine* phosphorylation signaling system, is clearly an innovation for which this domain had been recruited only in animals...

...domains, such as the intracellular domains (MATH, POZ, PDZ, and LIM), and the largely extracellular domains (FN3, LRR, and vWA); (ii) the phosphotyrosine signaling system-*tyrosine* kinases, phosphotyrosine *phosphatases*, SH2, and PTB (two types of phosphotyrosine-binding domains; the PTB domain was not detected in yeast); (iii) the cyclic nucleotide monophosphate (cNMP)-dependent signaling...

...Conclusions This first reciprocal analysis of two complete eukaryotic genome *sequences* has produced two kinds of results. First, it is clear that a comparable number of orthologous proteins carry out the core functions of both S...

...most of the signaling and regulatory genes known or expected to be involved in multicellularity have no yeast orthologs, even though they may contain domain *sequences* shared with yeast. Thus, virtually all biological processes characteristic of multicellular life are performed by proteins that are not close variants of proteins responsible forBoth of these conclusions depend strongly on having virtually complete *sequences* for both organisms. If only a fraction of the total *sequence* is known, there is no way to make inferences concerning failure to find a homolog. Likewise, if a comparable domain arrangement is not detected in an incomplete *sequence*, it is impossible to conclude that this domain arrangement is absent...

...Finally, the basic assumption that the so-called "model organisms" will provide reliable functional annotation for the human DNA *sequence* is strongly supported by our observations. First, the sum of the biology of worm and yeast can be obtained efficiently by studying core functions largely ...

... Begin Table : Columns 1 - 5 of 5

Caption:
Conservation of yeast and worm protein *sequences*. Two reciprocal BLASTP analyses were performed, first with each of the 6217 yeast ORFs as a query against the worm ORF dataset (19,099 ORFs) (yeast versus worm), and second with each worm ORF as a query against the yeast ORF data set (worm versus yeast). For each yeast query *sequence* with a significant BLASTP worm hit (based on a conservative P-value cutoff, see below) in the yeast-versus-worm analysis, a *sequence* group was formed by combining the yeast query with all of its worm hits. This list was augmented by adding the yeast hits produced by...

...a
query in the worm-versus-yeast BLASTP analysis, imposing the same P-value cutoff. Analogous groups were constructed by starting with each worm query *sequence* from the worm-versus-yeast analysis, again with the same P-value cutoff. All of the above *sequence* groups were processed together, removing redundant *sequences* within each group and coalescing different groups if they contained any common *sequence* or *sequences*. Within all groups collected for a given P-value data set, each yeast and worm *sequence* will occur only once. Different maximum P-value cutoffs were set for the initial collection of hits (1 x 10-10, 1 x 10-20, 1 x 10-50, and 1 x 10-100). *Sequence* groups were also constructed with the additional constraint that 80% or more of each query *sequence* be aligned; results were similar to those without the aligned length constraint and can be viewed on our Web site.

P-value	*Sequence* groups		Yeast ORFs (%)	Worm
			(n = 6217)	(%) (1909
	Total	>2 members		
1 x 10-100	236	79	330 (5.3)	370 (1.9)

1 x protein *sequences* were clustered into closely related groups (BLASTP P < 1 x 10.sup(-50), with the >80% aligned length constraint) as described in the legend to Table 1. Each *sequence* group (including groups with two or more *sequences*) was assigned into a single functional category, relying primarily on the functional annotations for the yeast genes in SGD when available (B44) . The unclassified category contains groups of *sequences* without annotation. The boxed number within each category reflects the ratio of worm to yeast proteins for that category...

...Figure Removed

Figure F2
Caption: Orthologous core biological functions in yeast and worm. Representative *sequence* groups are shown as rooted CLUSTALW Neighbor-Joining trees, clustered as described in the legend to Table 1, at a similarity level indicated after each...
...site. The axes show the number of proteins with the given domain per 1000 genes. 1, POZ domains; 2, EGF; 3, MATH domain; 4, phosphotyrosine *phosphatase*; 5, homeodomains; 6, leucine-rich repeats; 7, calmodulin; 8, PDZ domains; 9, voltage-gated channels; 10, ankyrin repeats; 11, RING domain; 12, C6 fingers; 13, nuclear hormone receptors; 14, AAA-type ATPases. The two domains that are most abundant in yeast, namely serine-*threonine* protein kinases and WD40 domains (Table 2), were not used for this plot, in order to improve resolution for the other points...

References and Notes:
...multiple domains that have a degree of evolutionary independence and are found in different combinations. Thus, the detection of even very high similarity between protein *sequences* from two species does not guarantee that the proteins in question are genuine orthologs with a conserved domain architecture (B10) . To diminish (but not eliminate...

...28 October version of the SGD (both are available from the Science Web site as well as SGD). Because the prediction of C. elegans protein *sequences* had, on 16 October, yet to be corrected by rigorous experimental analysis, our reliance on these predictions may result in the loss of some subset six frame translations of the entire worm DNA *sequence* (finished *sequence* from the Sanger Centre Web site as of 3 November 1998) and identified no additional homologs at the P < 10.sup(-10) level with the...

...14. Thompson, J. D., Higgins, D. G., Gibson, T. J., *Nucleic* *Acids* Res., 22 1994, 4673...though the similarity of these to RNA polymerases is, upon further study, clearly spurious. This artifact, due to low complexity in the Spt5p amino acid *sequence*, is avoidable by more aggressive filtering, applying the >80% alignment requirement as well as increasing the stringency; each of these measures exacts a cost in33. Altschul, S. F., et.al. *Nucleic* *Acids* Res., 25 1997, 3389 ...

...38. To obtain robust counts for each of the domains in the yeast and worm protein sets, we compared representative *sequences* of each domain to the nonredundant protein database (National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD) using the PSI-BLAST program, and the resulting position-dependent weight matrices (profiles) were saved. The number of search iterations and the cutoff for inclusion of *sequences* in the profile were adjusted individually for each domain. For most widespread domains, several profiles were constructed to ensure complete coverage. The profiles were then...the collaborations, and K. Anders for helpful discussions. We are especially grateful to R. Durbin (Sanger Centre) and L. Hillier (Genome Sequencing Center) for providing *sequence* information and for their cooperation. The SGD is supported by a P41 national resources grant HG01315, from the National Human Genome Research Institute at the...

8/3,K/3 (Item 3 from file: 370)
DIALOG(R)File 370:Science

00506906 (USE 9 FOR FULLTEXT)
Exploiting Chemical Libraries, Structure, and Genomics in the Search for Kinase Inhibitors
Gray, Nathanael S.; Wodicka, Lisa; Thunnissen, Andy-Mark W. H.; Norman, Thea C.; Kwon, Soojin; Espinoza, F. Hernan; Morgan, David O.; Barnes, Georjana; LeClerc, Sophie; Meijer, Laurent; Kim, Sung-Hou; Lockhart, David J.; Schultz, Peter G.
N. S. Gray, T. C. Norman, S. Kwon, P. G. Schultz, Howard Hughes Medical

Institute, University of California, Berkeley, CA 94720, USA. L. Wodicka and D. J. Lockhart, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA. A.-M. W. H. Thunnissen and S.-H. Kim, Lawrence Berkeley National Laboratory and Department of Chemistry, University of California, Berkeley, CA 94720, USA. F. Hernan Espinoza and D. O. Morgan, Department of Physiology, University of California, San Francisco, CA 94143-0444, USA. G. Barnes, Department of Molecular and Cellular Biology, University of California, Berkeley, CA 94720, USA. S. LeClerc and L. Meijer, CNRS, Station Biologique, 29682 Roscoff, France.
Science Vol. 281 5376 pp. 533
Publication Date: 7-24-1998 (980724) Publication Year: 1998
Document Type: Journal ISSN: 0036-8075
Language: English
Section Heading: Reports
Word Count: 4195

(THIS IS THE FULLTEXT)

...Text: to generate small molecule libraries using combinatorial chemistry methods coupled with high-throughput screening, (ii) the enormous increase in the number of newly identified gene *sequences* from a host of different organisms, and (iii) the use of structural methods for the detailed characterization of ligand-protein interaction sites that can be ...the acidic C8 atom of the purine ring and the carbonyl oxygen of Glu.sup(81), an infrequently observed interaction in the crystal structures of *nucleic* *acids* and proteins (B13...a positive feedback loop driving CLB1/2 transcription (B22) . Similarly, CDK activity has been implicated in transcriptional regulation of histone genes including HTA2 and HTB2 (*B23*) , and EGT2, a gene involved in the timing of cell separation after cytokinesis...

...on the Pho85p kinase complex to modulate the activity of a transcription factor or factors that regulate a variety of genes, including a secreted acid *phosphatase* (Pho5p) (B24) , genes involved in the stress response (the heat shock protein HSP12 and ubiquitin UBI4), and genes involved in glycogen metabolism. Proteins whose transcript...3,800

cGMP-dependent protein kinase	>10,000	>100,000
Casein kinase 1	>3,333	>3,333
GSK3- (beta)	>10,000	>10,000
Insulin-receptor *tyrosine* kinase	5,000	2,200
cCasein kinase 2	>10,000	>10,000
Raf kinase	>1,000	>10,000
v-abl	>10,000	>100,000

cdc28...

...YDR406w (PDR15); YDL223c (unknown); YER150w (similar to Sed1p an abundant cell surface glycoprotein); YGR032W (GSC2, component of (beta) -1,3-glucan synthase); YGL179C.sup(*) (serine-*threonine* kinase similar to Elm1p and Kin82p); YLR178C (TFS1, Cdc25-dependent nutrient and ammonia response cell cycle regulator); YNR009W (unknown); YFL031W (HAC1, basic leucine zipper protein...with Pho80p or Pho85p); YFL014W (HSP12, heat shock protein); YHR071W (PCL5, cyclinlike and associates with Pho85p); YGR088W (CTT1, cytosolic catalase T); YBR093c (PHO5, secreted acid *phosphatase*); YLL039c (UBI4, ubiquitin); YCL009c (PHO84, phosphate transporter); YML116W (PHO8, vacuolar alkaline *phosphatase*); YBR296c (homologous to a phosphate-repressible permease). (C) Transcripts that change for cdc28-4, cdc28-4 and 52, cdc28-4 and flavopiridol, and 52: YBR147W...

8/3,K/4 (Item 4 from file: 370)
DIALOG(R)File 370:Science

00501521 (USE 9 FOR FULLTEXT)
Inducible Expression and Phosphorylation of Coactivator BOB.1/OBF.1 in T Cells
Zwilling, Stefan; Dieckmann, Andreas; Pfisterer, Petra; Angel, Peter; Wirth, Thomas

S. Zwilling, P. Pfisterer, T. Wirth, MSZ, Institut fuer Medizinische Strahlenkunde und Zellforschung, Universitaet Wuerzburg, Versbacher Strasse 5, 97078 Wuerzburg, Germany. ; A. Dieckmann and P. Angel, DKFZ, Deutsches Krebsforschungszentrum, Abteilung Signaltransduktion und Wachstumskontrolle, Im Neuenheimer Feld 280, 69120 Heidelberg, Germany.
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(THIS IS THE FULLTEXT)

...Text: and Roeder, and they suggested that the 35-kD form might represent a modified version of the 34-kD polypeptide (B6) . Treatment of extracts with *phosphatases* did not convert the 35 kD band to the 34 kD band, however (B19...OBF.1 in B cells and T cells, respectively, are virtually identical (Fig. 4 , A and C). All of these phosphorylations occurred on serine and *threonine* residues, and no evidence for *tyrosine* phosphorylation was obtained (B22) . To determine whether the increased activity correlated with phosphorylation of the COOH-terminal domain, we performed an in vitro phosphorylation assay with the use of purified recombinant BOB.1/OBF.1 COOH-terminal fragment and extracts from unstimulated and stimulated Jurkat T cells (*B23*) . In extracts from unstimulated cells, low basal phosphorylation of the fragment encompassing the COOH-terminal 130 amino acids of BOB.1/OBF.1 was observed...

...Fig. 4). Exposure of cells to CsA or FK506 inhibited the effect of PMA and ionomycin. CsA and FK506 are inhibitors of the Ser/Thr-*phosphatase* calcineurin; therefore, calcineurin may be a component of the signal transduction pathway leading to the inducible phosphorylation of BOB.1/OBF.1. However, other potential...

...analysis of in vitro phosphorylated GST-BOB.C protein revealed that phosphorylation only occurred at serine residues, suggesting that the phosphorylation that was observed at *threonines* in full-length BOB.1/OBF.1 protein occurred within the NH.inf(2)-terminal part of the protein. The domain from amino acids 166...in induced (+) or uninduced (-) Jurkat cell extracts. The scheme (top) shows the COOH-terminal domain of the BOB.1/OBF.1 protein and highlights the *sequence* from amino acid 166 to 192, as well as the specific point mutations. (D) GAL4 fusion proteins containing the COOH-terminal 150 amino acids of...

References and Notes:
...19. BOB.1/OBF.1 was immunoprecipitated from B cell extracts or induced Jurkat T cell extracts, and precipitates were treated with calf intestinal alkaline *phosphatase* or (lambda) *phosphatase*. Efficient dephosphorylation was confirmed by including an in vitro phosphorylated protein in some of the samples. Subsequent analysis of the dephosphorylated immunoprecipitates did not show...

...mutated fragments of BOB.1/OBF.1 used for GAL fusion and GST fusion experiments were generated by polymerase chain reaction (PCR) amplification followed by *sequence* analysis. Details on the primers used are available upon request. The different subfragments were cloned in frame into either the expression vectors containing the DNA...26. Annweiler, A., Zwilling, S., Wirth, T., *Nucleic* *Acids* Res., 22 1994, 4250...